



SEQUENCE LISTING

<10> Seed, Brian
Aruffo, Alejandro
Camerini, David

<120> CD27 Coding Sequence

<130> 11-88L

<140> US 09/836,544

<141> 2001-04-17

<150> US 07/983,647

<151> 1992-12-01

<150> US 07/553,759

<151> 1990-07-13

<150> US 07/498,809

<151> 1990-03-23

<150> US 07/379,076

<151> 1989-07-13

<150> US 07/160,416

<151> 1988-02-25

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 2932

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence of expression vector, piH3

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atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc 180

ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc gataagtcgt 240
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 cgggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360
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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (7)..(1059)

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ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
15 20 25 30

ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
35 40 45

agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
50 55 60

tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
65 70 75

aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att 288
Lys Glu Lys Asp Thr Tyr Lys Lys Phe Lys Asn Gly Thr Leu Lys Ile
80 85 90

aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat 336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
95 100 105 110

gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att 384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
115 120 125

caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca 432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
130 135 140

acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg 480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
145 150 155

tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac 528

Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His
 160 165 170

aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac 576
 Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn
 175 180 185 190

aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa 624
 Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys
 195 200 205

ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc 672
 Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu
 210 215 220

ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa 720
 Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys
 225 230 235

aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac 768
 Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His
 240 245 250

aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct 816
 Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala
 255 260 265 270

tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct 864
 Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro
 275 280 285

ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac 912
 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
 290 295 300

cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca 960
 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
 305 310 315

caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag 1008
 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
 320 325 330

cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056
 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
 335 340 345 350

aat taaaaaagat agaaactgtc ttttcaata aaaagcactg tggatttctg 1109

Asn

ccctcctgat gtgcataatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
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<212> PRT
<213> Homo sapiens

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Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
35 40 45

Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
50 55 60

Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65 70 75 80

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
85 90 95

Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
100 105 110

Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
115 120 125

Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu

| | | | |
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| Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln | | | |
| 145 | 150 | 155 | 160 |
| Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp | | | |
| | 165 | 170 | 175 |
| Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val | | | |
| | 180 | 185 | 190 |
| Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu | | | |
| | 195 | 200 | 205 |
| Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met | | | |
| | 210 | 215 | 220 |
| Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln | | | |
| 225 | 230 | 235 | 240 |
| Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val | | | |
| | 245 | 250 | 255 |
| Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr | | | |
| | 260 | 265 | 270 |
| Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His | | | |
| | 275 | 280 | 285 |
| Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val | | | |
| | 290 | 295 | 300 |
| Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val | | | |
| 305 | 310 | 315 | 320 |
| His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys | | | |
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| Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn | | | |
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<211> 874

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> (13)..(723)

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Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
50 55 60

aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
65 70 75

aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
80 85 90

aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
95 100 105

att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
110 115 120 125

tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa 435
Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
130 135 140

tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr
145 150 155

tca tgg gat tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata 531
Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile
160 165 170

tat ttt aag atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt 579
Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu
175 180 185

agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt 627
Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys
190 195 200 205

atc cca agc agc ggt cat tca aga cac aga tat gca ctt ata ccc ata 675
Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile
210 215 220

cca tta gca gta att aca aca tgt att gtg ctg tat atg aat gtt ctt 723
Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu
225 230 235

taattgagaa gacaatttct tcatttttag gtattctgaa atgtgacaga aaaccagaca 783

gaaccaactc caattgattg gtaacagaag atgaagacaa cagcataact aaattatttt 843

aaaaactaaa aagccatctg atttctcatt t 874

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<211> 237
<212> PRT
<213> Homo sapiens

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20 25 30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp

| | | |
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| 100 | 105 | 110 |
| Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr | | |
| 115 | 120 | 125 |
| Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile | | |
| 130 | 135 | 140 |
| Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp | | |
| 145 | 150 | 155 |
| | | 160 |
| Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys | | |
| 165 | 170 | 175 |
| Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro | | |
| 180 | 185 | 190 |
| Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser | | |
| 195 | 200 | 205 |
| Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala | | |
| 210 | 215 | 220 |
| Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu | | |
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<211> 3900

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence of the piH3M vector.

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aatactgtcc ttctagtga gccgtagta ggccaccact tcaagaactc ttagcaccg 180

cctacatacc tcgctctgct aatcctgtta ccagtggctg ctgccagtgg cgataagtcg 240

tgtcttaccg ggttggaactc aagacgatag ttaccggata aggcgcagcg gtcgggctga 300

acgggggggtt cgtgcacaca gcccagcttg gagcgaacga cctacaccga actgagatac 360

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 cccatggctg actaattttt ttatttatg cagaggccga ggccgcctcg gcctctgagc 3840
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<211> 1514

<212> DNA

<213> Homo sapiens

<220>

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<222> (100)..(759)

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Met Leu Arg Leu Leu

1 5

ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag att 162

Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val Thr Gly Asn Lys Ile

10 15 20

ttg gtg aag cag tgc ccc atg ctt gta gcg tac gac aat gcg gtc aac 210

Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn Ala Val Asn

25 30 35

ctt agc tgc aag tat tcc tac aat ctc ttc tca agg gag ttc cgg gca 258
 Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu Phe Arg Ala
 40 45 50

tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat 306
 Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr
 55 60 65

ggg aat tac tcc cag cag ctt cag gtt tac tca aaa acg ggg ttc aac 354
 Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe Asn
 70 75 80 85

tgt gat ggg aaa ttg ggc aat gaa tca gtg aca ttc tac ctc cag aat 402
 Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr Leu Gln Asn
 90 95 100

ttg tat gtt aac caa aca gat att tac ttc tgc aaa att gaa gtt atg 450
 Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Glu Val Met
 105 110 115

tat cct cct cct tac cta gac aat gag aag agc aat gga acc att atc 498
 Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
 120 125 130

cat gtg aaa ggg aaa cac ctt tgt cca agt ccc cta ttt ccc gga cct 546
 His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
 135 140 145

tct aag ccc ttt tgg gtg ctg gtg gtg gtt ggt gga gtc ctg gct tgc 594
 Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
 150 155 160 165

tat agc ttg cta gta aca gtg gcc ttt att att ttc tgg gtg agg agt 642
 Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
 170 175 180

aag agg agc agg ctc ctg cac agt gac tac atg aac atg act ccc cgc 690
 Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
 185 190 195

cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc 738
 Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
 200 205 210

gac ttc gca gcc tat cgc tcc tgacacggac gcctatccag aagccagccg 789
 Asp Phe Ala Ala Tyr Arg Ser
 215 220

gctggcagcc cccatctgct caatatcact gctctggata ggaaatgacc gccatctcca 849
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agttc 1514

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<211> 220
<212> PRT
<213> Homo sapiens

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
 85 90 95
 Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
 100 105 110
 Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125
 Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140
 Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160
 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175
 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190
 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205
 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 9

<211> 1665

<212> DNA

<213> Homo sapiens

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ggggccctgg ctgccaagg taagagcttc ccaggctctc catggccaca gctccggagc 180

tctccctgcc ccatgagctc agagcccca gtctgagcca cagcacagcc cccaggaagc 240

gggtggggtg ctgagcggcc tccagtgtct gaggactcat ttaagagaag gaaaaagggt 300

ggacccggtg gggagtggcc ggggctgtcc aggcagggcc gctgcttgg gaggaagaag 360

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<210> 10

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 10

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (94)..(984)

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aggccttggg gactcaggag ttttgagagc aaa atg aca aca ccc aga aat tca 114
 Met Thr Thr Pro Arg Asn Ser

1 5

gta aat ggg act ttc ccg gca gag cca atg aaa ggc cct att gct atg 162
Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met
10 15 20

caa tct ggt cca aaa cca ctc ttc agg agg atg tct tca ctg gtg ggc 210
Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly
25 30 35

ccc acg caa agc ttc ttc atg agg gaa tct aag act ttg ggg gct gtc 258
Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val
40 45 50 55

cag att atg aat ggg ctc ttc cac att gcc ctg ggg ggt ctt ctg atg 306
Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met
60 65 70

atc cca gca ggg atc tat gca ccc atc tgt gtg act gtg tgg tac cct 354
Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro
75 80 85

ctc tgg gga ggc att atg tat att att tcc gga tca ctc ctg gca gca 402
Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala
90 95 100

acg gag aaa aac tcc agg aag tgt ttg gtc aaa gga aaa atg ata atg 450
Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met
105 110 115

aat tca ttg agc ctc ttt gct gcc att tct gga atg att ctt tca atc 498
Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile
120 125 130 135

atg gac ata ctt aat att aaa att tcc cat ttt tta aaa atg gag agt 546
Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser
140 145 150

ctg aat ttt att aga gct cac aca cca tat att aac ata tac aac tgt 594
Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys
155 160 165

gaa cca gct aat ccc tct gag aaa aac tcc cca tct acc caa tac tgt 642
Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys
170 175 180

tac agc ata caa tct ctg ttc ttg ggc att ttg tca gtg atg ctg atc 690
Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile
185 190 195

ttt gcc ttc ttc cag gaa ctt gta ata gct ggc atc gtt gag aat gaa 738
Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu
200 205 210 215

tgg aaa aga acg tgc tcc aga ccc aaa tct aac ata gtt ctc ctg tca 786
Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser
220 225 230

gca gaa gaa aaa aaa gaa cag act att gaa ata aaa gaa gaa gtg gtt 834
Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val
235 240 245

ggg cta act gaa aca tct tcc caa cca aag aat gaa gaa gac att gaa 882
Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
250 255 260

att att cca atc caa gaa gag gaa gaa gaa gaa aca gag acg aac ttt 930
Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe
265 270 275

cca gaa cct ccc caa gat cag gaa tcc tca cca ata gaa aat gac agc 978
Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser
280 285 290 295

tct cct taagtgttt cttctgttt ctgttcctt ttttaaacat tagtgttcat 1034
Ser Pro

agcttccaag agacatgctg actttcattt ctgaggtac tctgcacata cgcaccacat 1094

ctctatctgg cctttgcatg gagtgaccat agctccttct ctcttacatt gaatgtagag 1154

aatgtagcca tttagcagc ttgtgtgtc acgttcttc ttttagcaa ctttctaca 1214

ctgaagaaag gcagaatgag tgcttcagaa tgtgatttcc tactaacctg ttcttggat 1274

aggttttta gtatagtatt tttttgtc attttctcca tcagcaacca gggagactgc 1334

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<211> 297

<212> PRT

<213> Homo sapiens

<400> 12

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Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro

245 250 255
 Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
 260 265 270
 Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285
 Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 13
 <211> 1888
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (13)..(1608)

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 Leu Val Leu Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr
 15 20 25

tct gtg tcc ccc tca aaa gtc atc ctg ccc cgg gga ggc tcc gtg ctg 147
 Ser Val Ser Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu
 30 35 40 45

gtg aca tgc agc acc tcc tgt gac cag ccc aag ttg ttg ggc ata gag 195
 Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu
 50 55 60

acc ccg ttg cct aaa aag gag ttg ctc ctg cct ggg aac aac cgg aag 243
 Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys
 65 70 75

gtg tat gaa ctg agc aat gtg caa gaa gat agc caa cca atg tgc tat 291
 Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr
 80 85 90

tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc acc gtg 339
 Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val

95

100

105

tac tgg act cca gaa cgg gtg gaa ctg gca ccc ctc ccc tct tgg cag 387
 Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln
 110 115 120 125

cca gtg ggc aag aac ctt acc cta cgc tgc cag gtg gag ggt ggg gca 435
 Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala
 130 135 140

ccc cgg gcc aac ctc acc gtg gtg ctg ctc cgt ggg gag aag gag ctg 483
 Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu
 145 150 155

aaa cgg gag cca gct gtg ggg gag ccc gct gag gtc acg acc acg gtg 531
 Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val
 160 165 170

ctg gtg agg aga gat cac cat gga gcc aat ttc tcg tgc cgc act gaa 579
 Leu Val Arg Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu
 175 180 185

ctg gac ctg cgg ccc caa ggg ctg gag ctg ttt gag aac acc tcg gcc 627
 Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala
 190 195 200 205

ccc tac cag ctc cag acc ttt gtc ctg cca gcg act ccc cca caa ctt 675
 Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu
 210 215 220

gtc agc ccc cgg gtc cta gag gtg gac acg cag ggg acc gtg gtc tgt 723
 Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys
 225 230 235

tcc ctg gac ggg ctg ttc cca gtc tcg gag gcc cag gtc cac ctg gca 771
 Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala
 240 245 250

ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aac gac tcc 819
 Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser
 255 260 265

ttc tcg gcc aag gcc tca gtc agt gtg acc gca gag gac gag ggc acc 867
 Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr
 270 275 280 285

cag cgg ctg acg tgt gca gta ata ctg ggg aac cag agc cag gag aca 915
 Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr

| | | | |
|--|-----|-----|-----|
| 290 | 295 | 300 | |
| ctg cag aca gtg acc atc tac agc ttt ccg gcg ccc aac gtg att ctg 963 | | | |
| Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu | | | |
| 305 | 310 | 315 | |
| acg aag cca gag gtc tca gaa ggg acc gag gtg aca gtg aag tgt gag 1011 | | | |
| Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu | | | |
| 320 | 325 | 330 | |
| gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc cag cca 1059 | | | |
| Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro | | | |
| 335 | 340 | 345 | |
| ctg ggc ccg agg gcc cag ctc ctg ctg aag gcc acc cca gag gac aac 1107 | | | |
| Leu Gly Pro Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn | | | |
| 350 | 355 | 360 | 365 |
| ggg cgc agc ttc tcc tgc tct gca acc ctg gag gtg gcc gcc cag ctt 1155 | | | |
| Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu | | | |
| 370 | 375 | 380 | |
| ata cac aag aac cag acc cgg gag ctt cgt gtc ctg tat ggc ccc cga 1203 | | | |
| Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg | | | |
| 385 | 390 | 395 | |
| ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa aat tcc 1251 | | | |
| Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser | | | |
| 400 | 405 | 410 | |
| cag cag act cca atg tgc cag gct tgg ggg aac cca ttg ccc gag ctc 1299 | | | |
| Gln Gln Thr Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu | | | |
| 415 | 420 | 425 | |
| aag tgt cta aag gat ggc act ttc cca ctg ccc atc ggg gaa tca gtg 1347 | | | |
| Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val | | | |
| 430 | 435 | 440 | 445 |
| act gtc act cga gat ctt gag ggc acc tac ctc tgt cgg gcc agg agc 1395 | | | |
| Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser | | | |
| 450 | 455 | 460 | |
| act caa ggg gag gtc acc cgc gag gtg acc gtg aat gtg ctc tcc ccc 1443 | | | |
| Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro | | | |
| 465 | 470 | 475 | |
| cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc ata atg 1491 | | | |
| Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met | | | |

480 485 490

ggc act gca ggc ctc agc acg tac ctc tat aac cgc cag cgg aag atc 1539
Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile
495 500 505

aag aaa tac aga cta caa cag gcc caa aaa ggg acc ccc atg aaa ccg 1587
Lys Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro
510 515 520 525

aac aca caa gcc acg cct ccc tgaacctatc ccgggacagg gcctcttctt 1638
Asn Thr Gln Ala Thr Pro Pro
530

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<211> 532

<212> PRT

<213> Homo sapiens

<400> 14

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35 40 45

Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
50 55 60

Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
65 70 75 80

Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
85 90 95

Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
100 105 110

Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
115 120 125

Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
130 135 140

Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
145 150 155 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
165 170 175

Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
180 185 190

Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
195 200 205

Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
210 215 220

Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
225 230 235 240

Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
245 250 255

Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
260 265 270

Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
275 280 285

Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
290 295 300

Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
305 310 315 320

Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
325 330 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
340 345 350

Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
355 360 365

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
370 375 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
385 390 395 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
405 410 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
420 425 430

Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
450 455 460

Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
465 470 475 480

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
485 490 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
500 505 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
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<211> 1922

<212> DNA

<213> Homo sapiens

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aa

1922

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 <211> 1476
 <212> DNA
 <213> Homo sapiens

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 <211> 2290
 <212> DNA
 <213> Homo sapiens

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<210> 18
<211> 2171
<212> DNA
<213> Homo sapiens

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<210> 19

<211> 1004

<212> DNA
<213> Homo sapiens

<400> 19

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<210> 20
<211> 1870
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (211)..(1626)

<400> 20

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gaaccagagc ttgtagaaac cactttaatc atatccagga gtttgcaaga aacaggtgct 180

taacactaat tcacctcctg aacaagaaaa atg ggc tgt gac cgg aac tgt ggg 234

Met Gly Cys Asp Arg Asn Cys Gly

1 5

ctc atc gct ggg gct gtc att ggt gct gtc ctg gct gtg ttt gga ggt 282

Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly

10 15 20

att cta atg cca gtt gga gac ctg ctt atc cag aag aca att aaa aag 330

Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys

25 30 35 40

caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa 378

Gln Val Val Leu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys

45 50 55

aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat 426

Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn

60 65 70

cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga 474

Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg

75 80 85

ggt cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc 522

Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr

90 95 100

cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc 570

Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala

105 110 115 120

atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca 618

Ile Phe Glu Pro Ser Leu Ser Val Gly Thr Glu Ala Asp Asn Phe Thr

125 130 135

gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa 666

Val Leu Asn Leu Ala Val Ala Ala Ala Ser His Ile Tyr Gln Asn Gln

140 145 150

ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct 714

Phe Val Gln Met Ile Leu Asn Ser Leu Ile Asn Lys Ser Lys Ser Ser
155 160 165

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170 175 180

cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg 810
Pro Phe Leu Ser Leu Val Pro Tyr Pro Val Thr Thr Val Gly Leu
185 190 195 200

ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat 858
Phe Tyr Pro Tyr Asn Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn
205 210 215

gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt 906
Gly Lys Asp Asn Ile Ser Lys Val Ala Ile Ile Asp Thr Tyr Lys Gly
220 225 230

aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt 954
Lys Arg Asn Leu Ser Tyr Trp Glu Ser His Cys Asp Met Ile Asn Gly
235 240 245

aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg 1002
Thr Asp Ala Ala Ser Phe Pro Pro Phe Val Glu Lys Ser Gln Val Leu
250 255 260

cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa 1050
Gln Phe Phe Ser Ser Asp Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu
265 270 275 280

tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca 1098
Ser Asp Val Asn Leu Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro
285 290 295

tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc 1146
Ser Lys Ala Phe Ala Ser Pro Val Glu Asn Pro Asp Asn Tyr Cys Phe
300 305 310

tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta 1194
Cys Thr Glu Lys Ile Ile Ser Lys Asn Cys Thr Ser Tyr Gly Val Leu
315 320 325

gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct 1242
Asp Ile Ser Lys Cys Lys Glu Gly Arg Pro Val Tyr Ile Ser Leu Pro
330 335 340

cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta 1290

38

Met Gly Cys Asp Arg Asn Cys Gly Leu Ile Ala Gly Ala Val Ile Gly
 1 5 10 15
 Ala Val Leu Ala Val Phe Gly Gly Ile Leu Met Pro Val Gly Asp Leu
 20 25 30
 Leu Ile Gln Lys Thr Ile Lys Lys Gln Val Val Leu Glu Glu Gly Thr
 35 40 45
 Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln
 50 55 60
 Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser
 65 70 75 80
 Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg
 85 90 95
 Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val
 100 105 110
 Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val
 115 120 125
 Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala
 130 135 140
 Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser
 145 150 155 160
 Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg
 165 170 175
 Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr
 180 185 190
 Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala
 195 200 205
 Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val
 210 215 220
 Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu
 225 230 235 240
 Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro
 245 250 255

Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys
260 265 270

Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile
275 280 285

Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val
290 295 300

Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys
305 310 315 320

Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly
325 330 335

Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp
340 345 350

Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg
355 360 365

Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala
370 375 380

Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln
385 390 395 400

Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu
405 410 415

Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser
420 425 430

Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu
435 440 445

Leu Ser Val Gly Val Val Met Phe Val Ala Phe Met Ile Ser Tyr Cys
450 455 460

Ala Cys Arg Ser Lys Thr Ile Lys
465 470

<210> 22

<211> 1321

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)..(1158)

<400> 22

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Met Trp Phe Leu Thr Thr

1 5

ctg ctc ctt tgg gtt cca gtt gat ggg caa gtg gac acc aca aag gca 102

Leu Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala

10 15 20

gtg atc tct ttg cag cct cca tgg gtc agc gtg ttc caa gag gaa acc 150

Val Ile Ser Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr

25 30 35

gta acc ttg cac tgt gag gtg ctc cat ctg cct ggg agc agc tct aca 198

Val Thr Leu His Cys Glu Val Leu His Leu Pro Gly Ser Ser Ser Thr

40 45 50

cag tgg ttt ctc aat ggc aca gcc act cag acc tcg acc ccc agc tac 246

Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln Thr Ser Thr Pro Ser Tyr

55 60 65 70

aga atc acc tct gcc agt gtc aat gac agt ggt gaa tac agg tgc cag 294

Arg Ile Thr Ser Ala Ser Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln

75 80 85

aga ggt ctc tca ggg cga agt gac ccc ata cag ctg gaa atc cac aga 342

Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile Gln Leu Glu Ile His Arg

90 95 100

ggc tgg cta cta ctg cag gtc tcc agc aga gtc ttc acg gaa gga gaa 390

Gly Trp Leu Leu Leu Gln Val Ser Ser Arg Val Phe Thr Glu Gly Glu

105 110 115

cct ctg gcc ttg agg tgt cat gcg tgg aag gat aag ctg gtg tac aat 438

Pro Leu Ala Leu Arg Cys His Ala Trp Lys Asp Lys Leu Val Tyr Asn

120 125 130

gtg ctt tac tat cga aat ggc aaa gcc ttt aag ttt ttc cac tgg aat 486

Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe Lys Phe Phe His Trp Asn

135 140 145 150

tct aac ctc acc att ctg aaa acc aac ata agt cac aat ggc acc tac 534

Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile Ser His Asn Gly Thr Tyr

155 160 165

cat tgc tca ggc atg gga aag cat cgc tac aca tca gca gga ata tct 582
His Cys Ser Gly Met Gly Lys His Arg Tyr Thr Ser Ala Gly Ile Ser
170 175 180

gtc act gtg aaa gag cta ttt cca gct cca gtg ctg aat gca tct gtg 630
Val Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val
185 190 195

aca tcc cca ctc ctg gag ggg aat ctg gtc acc ctg agc tgt gaa aca 678
Thr Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr
200 205 210

aag ttg ctc ttg cag agg cct ggt ttg cag ctt tac ttc tcc ttc tac 726
Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr
215 220 225 230

atg ggc agc aag acc ctg cga ggc agg aac aca tcc tct gaa tac caa 774
Met Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln
235 240 245

ata cta act gct aga aga gaa gac tct ggg tta tac tgg tgc gag gct 822
Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala
250 255 260

gcc aca gag gat gga aat gtc ctt aag cgc agc cct gag ttg gag ctt 870
Ala Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu
265 270 275

caa gtg ctt ggc ctc cag tta cca act cct gtc tgg ttt cat gtc ctt 918
Gln Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu
280 285 290

ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg 966
Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp
295 300 305 310

gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa 1014
Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Asp Leu Glu
315 320 325

atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa 1062
Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln
330 335 340

gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa 1110
Glu Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu
345 350 355

gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg 1158
 Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr
 360 365 370

tagcagcggc tcagtgggtg gccatcgatc tggaccgtcc cctgccact tgctccccgt 1218

gagcactgcg tacaaacatc caaaagtca acaacaccag aactgtgtgt ctcatggtat 1278

gtaactctta aagcaaataa atgaactgac ttcaaaaaaa aaa 1321

<210> 23

<211> 374

<212> PRT

<213> Homo sapiens

<400> 23

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
 1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Ser Leu Gln Pro Pro Trp Val Ser
 20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
 35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
 50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
 65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
 85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
 100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
 115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
 130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
 145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
275 280 285

Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
290 295 300

Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
305 310 315 320

Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
325 330 335

Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys
340 345 350

Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys
355 360 365

Glu Pro Gln Gly Ala Thr
370

<210> 24

<211> 1714

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (156)..(1163)

<400> 24

gcggggagct tgcagtgacc aagagggtgt tgaggctagg aggccacgat aaacaggata 60

cgataaaagt ccttaaccaa gacgcagatg ggaagaagcg ttagagcgag cagcactcac 120

atctcaagaa ccagcctttc aaacagtttc cagag atg gat tat cct act tta 173

Met Asp Tyr Pro Thr Leu

1 5

ctt ttg gct ctt ctt cat gta tac aga gct cta tgt gaa gag gtg ctt 221

Leu Leu Ala Leu Leu His Val Tyr Arg Ala Leu Cys Glu Glu Val Leu

10 15 20

tgg cat aca tca gtt ccc ttt gcc gag aac atg tct cta gaa tgt gtg 269

Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser Leu Glu Cys Val

25 30 35

tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg 317

Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly

40 45 50

acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc 365

Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val

55 60 65 70

ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg 413

Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met

75 80 85

gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat 461

Ala Ser Asn Asn Met Thr Leu Phe Arg Asn Ala Ser Glu Asp Asp

90 95 100

gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg 509

Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp

105 110 115

cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg 557

Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe Glu Ala Ala Val

120 125 130

cca tca aat agc cac att gtt tgc gaa cct gga aag aat gtc aca etc 605

Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu

135 140 145 150

act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa 653
 Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu
 155 160 165

aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc 701
 Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val
 170 175 180

cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac 749
 His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn
 185 190 195

tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc 797
 Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val
 200 205 210

tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa 845
 Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu
 215 220 225 230

aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat 893
 Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp
 235 240 245

aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg 941
 Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu Leu
 250 255 260

ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg 989
 Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg
 265 270 275

aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag 1037
 Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln
 280 285 290

aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc 1085
 Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr
 295 300 305 310

aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca 1133
 Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro
 315 320 325

acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga 1183
 Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 330 335

gtgcattagt aatgactctt atgtactcat gcatggatct ttatgaatt ttttccact 1243
 acccaaggtc taccttagat actagttgtc tgaattgagt tactttgata ggaaaaatac 1303
 ttcatcactt aaaatcattt tcatagaac tgttcagaa aacctgactc taactggttt 1363
 atatacaaaa gaaaacttac tgtatcatat aacagaatga tccaggggag attaagcttt 1423
 gggcaagggc tatttaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac 1483
 tggtcttga atccctttcc agagtgttg atccatttcc ctggtcttgg cctcactctc 1543
 atgcaggctt tctcttgtg ttggcaagat ggctgccaac tcttggcaat tcatacatcc 1603
 ttgtttctgt ctggtagaga gtttgcctt caaatggagc aaacaaattt gattattttt 1663
 tcattgttaa ataggcaaca tgaccataaa ggatggaatg gcttaagtaa a 1714

<210> 25
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
 1 5 10 15
 Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
 20 25 30
 Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
 35 40 45
 Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
 50 55 60
 Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
 65 70 75 80
 Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
 85 90 95
 Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
 100 105 110
 Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp

| | | |
|---|-----|-----|
| 115 | 120 | 125 |
| Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro | | |
| 130 | 135 | 140 |
| Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val | | |
| 145 | 150 | 155 |
| | | 160 |
| Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu | | |
| 165 | 170 | 175 |
| Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro | | |
| 180 | 185 | 190 |
| Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val | | |
| 195 | 200 | 205 |
| Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu | | |
| 210 | 215 | 220 |
| Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val | | |
| 225 | 230 | 235 |
| | | 240 |
| Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly | | |
| 245 | 250 | 255 |
| Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val | | |
| 260 | 265 | 270 |
| Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr | | |
| 275 | 280 | 285 |
| Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile | | |
| 290 | 295 | 300 |
| Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp | | |
| 305 | 310 | 315 |
| | | 320 |
| Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val | | |
| 325 | 330 | 335 |

<210> 26
 <211> 2107
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> (35)..(1975)

<400> 26

acgcggaaac aggcctgcac ccagacacga cacc atg cat ctc ctc ggc ccc tgg 55
Met His Leu Leu Gly Pro Trp
1 5

ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103
Leu Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys
10 15 20

tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151
Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys
25 30 35

gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199
Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser
40 45 50 55

ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tcg aag ttt 247
Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe
60 65 70

gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295
Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser
75 80 85

gag cag aaa agg gtg caa ttc ctg gga gac aag aat aag aac tgc aca 343
Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn Lys Asn Cys Thr
90 95 100

ctg agt atc cac ccg gtg cac ctc aat gac agt ggt cag ctg ggg ctg 391
Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly Gln Leu Gly Leu
105 110 115

agg atg gag tcc aag act gag aaa tgg atg gaa cga ata cac ctc aat 439
Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg Ile His Leu Asn
120 125 130 135

gtc tct gaa agg cct ttt cca cct cat atc cag ctc cct cca gaa att 487
Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu Pro Pro Glu Ile
140 145 150

caa gag tcc cag gaa gtc act ctg acc tgc ttg ctg aat ttc tcc tgc 535
Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu Asn Phe Ser Cys
155 160 165

tat ggg tat ccg atc caa ttg cag tgg ctc cta gag ggg gtt cca atg 583
Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu Gly Val Pro Met
170 175 180

agg cag gct gct gtc acc tcg acc tcc ttg acc atc aag tct gtc ttc 631
Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile Lys Ser Val Phe
185 190 195

acc cgg agc gag ctc aag ttc tcc cca cag tgg agt cac cat ggg aag 679
Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser His His Gly Lys
200 205 210 215

att gtg acc tgc cag ctt cag gat gca gat ggg aag ttc ctc tcc aat 727
Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys Phe Leu Ser Asn
220 225 230

gac acg gtg cag ctg aac gtg aag cat cct ccc aag aag gtg acc aca 775
Asp Thr Val Gln Leu Asn Val Lys His Pro Pro Lys Lys Val Thr Thr
235 240 245

gtg att caa aac ccc atg ccg att cga gaa gga gac aca gtg acc ctt 823
Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu
250 255 260

tcc tgt aac tac aat tcc agt aac ccc agt gtt acc cgg tat gaa tgg 871
Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp
265 270 275

aaa ccc cat ggc gcc tgg gag gag cca tcg ctt ggg gtg ctg aag atc 919
Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile
280 285 290 295

caa aac gtt ggc tgg gac aac aca acc atc gcc tgc gca gct tgt aat 967
Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Ala Cys Asn
300 305 310

agt tgg tgc tcg tgg gcc tcc cct gtc gcc ctg aat gtc cag tat gcc 1015
Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala
315 320 325

ccc cga gac gtg agg gtc cgg aaa atc aag ccc ctt tcc gag att cac 1063
Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His
330 335 340

tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc 1111
Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro
345 350 355

aaa gaa gtc cag ttc ttc tgg gag aaa aat ggc agg ctt ctg ggg aaa 1159
 Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys
 360 365 370 375

gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt 1207
 Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser
 380 385 390

tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc 1255
 Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala
 395 400 405

tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg 1303
 Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met
 410 415 420

agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt 1351
 Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys
 425 430 435

gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg 1399
 Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp
 440 445 450 455

aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg 1447
 Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro
 460 465 470

gtg aag gtc cag cac tcg ggt gcc tac tgg tgc cag ggg acc aac agt 1495
 Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser
 475 480 485

gtg ggc aag ggc cgt tcg cct ctc agc acc ctc acc gtc tac tat agc 1543
 Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser
 490 495 500

ccg gag acc atc ggc agg cga gtg gct gtg gga ctc ggg tcc tgc ctc 1591
 Pro Glu Thr Ile Gly Arg Arg Val Ala Val Gly Leu Gly Ser Cys Leu
 505 510 515

gcc atc ctc atc ctg gca atc tgt ggg ctc aag ctc cag cga cgt tgg 1639
 Ala Ile Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp
 520 525 530 535

aag agg aca cag agc cag cag ggg ctt cag gag aat tcc agc ggc cag 1687
 Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln
 540 545 550

agc ttc ttt gtg agg aat aaa aag gtt aga agg gcc ccc ctc tct gaa 1735
 Ser Phe Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu
 555 560 565

ggc ccc cac tcc ctg gga tgc tac aat cca atg atg gaa gat ggc att 1783
 Gly Pro His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile
 570 575 580

agc tac acc acc ctg cgc ttt ccc gag atg aac ata cca cga act gga 1831
 Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly
 585 590 595

gat gca gag tcc tca gag atg cag aga cct ccc ccg gac tgc gat gac 1879
 Asp Ala Glu Ser Ser Glu Met Gln Arg Pro Pro Pro Asp Cys Asp Asp
 600 605 610 615

acg gtc act tat tca gca ttg cac aag cgc caa gtg ggc act atg aga 1927
 Thr Val Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Thr Met Arg
 620 625 630

acg tca ttc cag att ttc cag aag atg agg gga ttc att act cag agc 1975
 Thr Ser Phe Gln Ile Phe Gln Lys Met Arg Gly Phe Ile Thr Gln Ser
 635 640 645

tgatccagtt tggggctcggg gagcggcctc aggcacaaga aaatgtggac tatgtgatcc 2035

tcaaacattg aacttgatg ggctgcagca gaggcactgg gggcagcggg ggccagggaa 2095

gtcccccagtt tt 2107

<210> 27

<211> 647

<212> PRT

<213> Homo sapiens

<400> 27

Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
 1 5 10 15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
 20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
 35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
 50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
 85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
 100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
 115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
 130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
 165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
 180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
 195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
 210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
225 230 235 240

Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg
 245 250 255

Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro
 260 265 270

Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro
 275 280 285

Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr
 290 295 300

Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val
305 310 315 320

Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile
325 330 335

Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys
340 345 350

Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys
355 360 365

Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile
370 375 380

Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile
385 390 395 400

Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro
405 410 415

Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly
420 425 430

Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser
435 440 445

His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser
450 455 460

Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr
465 470 475 480

Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser
485 490 495

Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala
500 505 510

Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly
515 520 525

Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu
530 535 540

Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val
545 550 555 560

Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn
565 570 575

Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu
580 585 590

Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg
595 600 605

Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys
610 615 620

Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met
625 630 635 640

Arg Gly Phe Ile Thr Gln Ser
645

<210> 28

<211> 1200

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)..(880)

<400> 28

ggggtgcaaa gaagagacag cagcgcccag cttggaggtg ctaactccag aggccagcat 60

cagcaactgg gcacagaaag gagccgcctg ggcagggacc atg gca cgg cca cat 115
Met Ala Arg Pro His
1 5

ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act 163
Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr
10 15 20

cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag 211
Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys
25 30 35

ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt 259
Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys
40 45 50

gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc 307
Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val
55 60 65

tcc ttc tct cct gac cac cac acc cgg ccc cac tgt gag agc tgt cgg 355
 Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg
 70 75 80 85

cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat 403
 His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn
 90 95 100

gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc 451
 Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys
 105 110 115

acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct 499
 Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser
 120 125 130

cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt 547
 Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser
 135 140 145

gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac 595
 Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp
 150 155 160 165

ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa 643
 Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln
 170 175 180

aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct 691
 Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser
 185 190 195

gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa 739
 Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln
 200 205 210

cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca 787
 Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala
 215 220 225

gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc 835
 Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr Ile
 230 235 240 245

ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc 880
 Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
 250 255 260

tgagccagca cctgcggtag ctgcactaca gccctggcct ccacccccac cccgccgacc 940
 atccaaggga gaggtagacc tggcagccac aactgcagtc ccatcctctt gtcagggccc 1000
 ttctctgtgt acacgtgaca gaggccttt tcgagactgg cagggacgag gacaaatatg 1060
 gatgaggtgg agagtgggaa gcaggagccc agccagctgc gcgcgcgtgc aggagggcgg 1120
 gggctctggt tgtaaggcac acttctctgt gcgaaagacc cacatgctac aagacgggca 1180
 aaataaagtg acagatgacc 1200

<210> 29
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
 1 5 10 15
 Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
 20 25 30
 Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
 35 40 45
 Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
 50 55 60
 Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
 65 70 75 80
 Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
 85 90 95
 Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
 100 105 110
 Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
 115 120 125
 Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
 130 135 140
 Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met

145 150 155 160
 Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
 165 170 175
 His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
 180 185 190
 Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
 195 200 205
 Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
 210 215 220
 Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu
 225 230 235 240
 Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
 245 250 255
 Ala Cys Ser Pro
 260

<210> 30
 <211> 2350
 <212> DNA
 <213> Homo sapiens

<400> 30
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 aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgac agagcaccca 120
 gagggactta tggaacatct tcaagttgtg ggggtggaca atgctctgtt gtgatttctt 180
 ggcacatcat ggaaccgact gctggactta ccattattct gaaaaacca tgaactggca 240
 aagggctaga agattctgcc gagacaatta cacagattta gttgccatac aaaacaaggc 300
 ggaaattgag tatctggaga agactctgcc tttagctgt tcttactact ggataggaat 360
 ccggaagata ggaggaatat ggacgtgggt gggaaccaac aaatctctca ctgaagaagc 420
 agagaactgg ggagatggtg agcccaacaa caagaagaac aaggaggact gcgtggagat 480
 ctatatcaag agaaacaaag atgcaggcaa atggaacgat gacgcctgcc acaactaaa 540

ggcagccctc tgttacacag ctcttgcca gccctggta tgcagtggcc atggagaatg 600
 tgtagaaatc atcaataatt acacctgcaa ctgtgatgtg gggactatg ggccccagtg 660
 tcagtttgtg attcagtgtg agcctttgga ggccccagag ctgggtacca tggactgtac 720
 tcactctttg ggaaacttca gcttcagctc acagtgtgcc ttcagctgct ctgaaggaac 780
 aaacttaact gggatigaag aaaccacctg tggaccattt ggaaactggt catctccaga 840
 accaacctgt caagtattc agtgtgagcc tctatcagca ccagattgg ggatcatgaa 900
 ctgtagccat cccctggcca gcttcagctt tacctctgca tgtaccttca tctgctcaga 960
 aggaactgag ttaattggga agaagaaaac catttgtgaa tcactggaa tctggtcaaa 1020
 tcctagtcca atatgtcaaa aattggacaa aagtttctca atgattaagg aggggtgatta 1080
 taacccctc ttattccag tggcagtcac ggttactgca ttctctgggt tggcattat 1140
 catttgctg gcaaggagat taaaaaagg caagaaatcc aagagaagta tgaatgacc 1200
 atattaaatc gcccttggtg aaagaaaatt ctggaatac taaaaatcat gagatcctt 1260
 aaatccttc atgaaacgtt ttgtgtggtg gcacctccta cgtcaaaca gaagtgtgtt 1320
 tccttcagt catctgggaa gatttctacc tgaccaacag ttcttcagc ttccattcg 1380
 cccctcatt atccctcaac cccagccca caggtgttta tacagctcag cttttgtct 1440
 ttctgagga gaaacaaata agaccataaa gggaaaggat tcatgtggaa tataaagatg 1500
 gctgactttg ctcttcttg actctgttt tcagttcaa ttcagtgtg tacttgatga 1560
 cagacacttc taaatgaagt gcaaatttga tacatatgtg aatatggact cagtttctt 1620
 gcagatcaaa tttcacgtcg tcttctgtat actgtggagg tacacttta tagaaagtc 1680
 aaaaagtcta cgctctcct tcttctaac tccagtgaag taatggggtc ctgctcaagt 1740
 tgaaagagtc ctattgcac ttagcctcg ccgtctgtga attggacat cctatttaac 1800
 tggcttcagc ctccccact tcttcagcca cctctcttt tcagttggct gacttcaca 1860
 cctagcatct catgagtcc aagcaaaagg agagaagaga gaaatagcct gcgctgttt 1920
 ttagtggg ggtttgctg ttctcttta tgagacccat tctatttct tatagtcaat 1980

gtttctttta tcacgatatt attagtaaga aaacatcact gaaatgctag ctgcaagtga 2040
catctctttg atgtcatatg gaagagttaa aacaggtgga gaaattcctt gattcacaat 2100
gaaatgctct cctttccctt gccccagac cttttatccg acttacctag attctacata 2160
ttctttaaatt ttcattcag gcctccctca accccaccac ttctttata actagtcctt 2220
tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2280
acatgcaatt ttgcatttga ataaagcctg cttttaagt gttaaaaaaa aaaaaaaaaa 2340
aaaaaaaaaa 2350

<210> 31
<211> 1354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (116)..(1198)

<400> 31
ccagcctctg ccaggttcgg tccgccatcc tegtcccgtc ctccgccggc cctgccccg 60
cgcccaggga tctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg 118
Met
1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358

Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
 70 75 80
 ata gaa ggg cat gtg gtg att ccc egg atc cac ccc aac tcc atc tgt 406
 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
 85 90 95
 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
 100 105 110
 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
 115 120 125
 aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550
 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
 130 135 140 145
 act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598
 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr
 150 155 160
 aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac 646
 Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp
 165 170 175
 gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac 694
 Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr
 180 185 190
 atc ttt tac acc ttt tet act gta cac ccc atc cca gac gaa gac agt 742
 Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser
 195 200 205
 ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa 790
 Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln
 210 215 220 225
 gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa 838
 Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu
 230 235 240
 tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc 886
 Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr
 245 250 255
 tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg 934

Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu
260 265 270

gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc 982
Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val
275 280 285

aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt 1030
Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser
290 295 300 305

ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag 1078
Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu
310 315 320

gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca 1126
Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser
325 330 335

gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag 1174
Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln
340 345 350

aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaagaaa 1228
Asn Val Asp Met Lys Ile Gly Val
355 360

caaccgttgt aaacataacc attacaggga gctgggacac ttaacagatg caatgtgcta 1288

ctgattgttt cattgcgaat ctttttagc ataaaatttt ctactctttt tgtaaaaaa 1348

aaaaaa 1354

<210> 32

<211> 361

<212> PRT

<213> Homo sapiens

<400> 32

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
210 215 220

Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
225 230 235 240

Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
245 250 255

Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
260 265 270

Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
275 280 285

Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn
290 295 300

Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly
 305 310 315 320

Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser
 325 330 335

Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu
 340 345 350

Gln Asn Val Asp Met Lys Ile Gly Val
 355 360

<210> 33

<211> 2308

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1594)

<400> 33

ccagcctctg ccaggttcgg tccgccatcc tcgtcccgct ctccgccggc ccctgccccg 60

cgcccaggga tctccagct cctttgccc ggcgcctcgg ttcgctcggg acacc atg 118
 Met
 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe

| | | | |
|---|-----|-----|-----|
| 70 | 75 | 80 | |
| ata gaa ggg cat gtg gtg att ccc egg atc cac ccc aac tcc atc tgt 406 | | | |
| Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys | | | |
| 85 | 90 | 95 | |
| gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454 | | | |
| Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln | | | |
| 100 | 105 | 110 | |
| tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502 | | | |
| Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys | | | |
| 115 | 120 | 125 | |
| aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550 | | | |
| Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile | | | |
| 130 | 135 | 140 | 145 |
| act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598 | | | |
| Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr | | | |
| 150 | 155 | 160 | |
| aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac 646 | | | |
| Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp | | | |
| 165 | 170 | 175 | |
| gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac 694 | | | |
| Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr | | | |
| 180 | 185 | 190 | |
| atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt 742 | | | |
| Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser | | | |
| 195 | 200 | 205 | |
| ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat atg gac 790 | | | |
| Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met Asp | | | |
| 210 | 215 | 220 | 225 |
| tcc agt cat agt aca acg ctt cag cct act gca aat cca aac aca ggt 838 | | | |
| Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly | | | |
| 230 | 235 | 240 | |
| ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca acg cag 886 | | | |
| Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr Gln | | | |
| 245 | 250 | 255 | |
| cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg gaa gaa 934 | | | |
| Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu Glu | | | |

| | | | |
|--|-----|-----|-----|
| 260 | 265 | 270 | |
| gat aaa gac cat cca aca act tct act ctg aca tca agc aat agg aat 982 | | | |
| Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn | | | |
| 275 | 280 | 285 | |
| gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc tca act 1030 | | | |
| Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser Thr | | | |
| 290 | 295 | 300 | 305 |
| cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc 1078 | | | |
| His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu Ser | | | |
| 310 | 315 | 320 | |
| agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt 1126 | | | |
| Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val | | | |
| 325 | 330 | 335 | |
| act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta 1174 | | | |
| Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu | | | |
| 340 | 345 | 350 | |
| tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act 1222 | | | |
| Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr | | | |
| 355 | 360 | 365 | |
| cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga 1270 | | | |
| His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly | | | |
| 370 | 375 | 380 | 385 |
| gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg 1318 | | | |
| Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp | | | |
| 390 | 395 | 400 | |
| ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt 1366 | | | |
| Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val | | | |
| 405 | 410 | 415 | |
| tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta 1414 | | | |
| Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu | | | |
| 420 | 425 | 430 | |
| gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga 1462 | | | |
| Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly | | | |
| 435 | 440 | 445 | |
| ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac 1510 | | | |
| Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn | | | |

450 455 460 465
 aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca 1558
 Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr
 470 475 480
 agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac 1604
 Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
 485 490
 accattatct tggaagaaa caacgttgga aacataacca ttacagggga gctgggacac 1664
 ttaacagatg caatgtgcta ctgattgttt cattcgaat ctataatagc ataaaatttt 1724
 ctactctttt tgtttttgt gttttgttct ttaaagtcag gtccaatttg taaaaacagc 1784
 attgctttct gaaattaggg cccaattaat aatcagcaag aattttgatc gtttcagttc 1844
 cccacttgga ggcctttcat cctcgggtg tgctatggat ggcttctaac aaaaacctac 1904
 cacatagtta ttctgatcg ccaaccttgc cccccaccag ctaaggacat ttccagggtt 1964
 aatagggcct ggtcctggga ggaaattga atgggtcatt ttgcccttcc attagcctaa 2024
 tcctgggca ttgctttcca ctgaggttg gggttgggt gtactagtta cacatcttca 2084
 acagaccccc tctagaaatt ttccagatgc ttctgggaga cacccaaagg gtaagtctat 2144
 ttatctgtag taaactattt atctgtgttt tgaaatatt aaacctgga tcagtccttt 2204
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<210> 34
 <211> 493
 <212> PRT
 <213> Homo sapiens

<400> 34
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 1 5 10 15
 Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30
 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu

| | | | |
|---|-----|-----|-----|
| 35 | 40 | 45 | |
| Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala | | | |
| 50 | 55 | 60 | |
| Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly | | | |
| 65 | 70 | 75 | 80 |
| Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile | | | |
| 85 | 90 | 95 | |
| Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser | | | |
| 100 | 105 | 110 | |
| Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp | | | |
| 115 | 120 | 125 | |
| Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr | | | |
| 130 | 135 | 140 | |
| Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu | | | |
| 145 | 150 | 155 | 160 |
| Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp | | | |
| 165 | 170 | 175 | |
| Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly | | | |
| 180 | 185 | 190 | |
| Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp | | | |
| 195 | 200 | 205 | |
| Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met | | | |
| 210 | 215 | 220 | |
| Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr | | | |
| 225 | 230 | 235 | 240 |
| Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr | | | |
| 245 | 250 | 255 | |
| Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu | | | |
| 260 | 265 | 270 | |
| Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg | | | |
| 275 | 280 | 285 | |
| Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser | | | |

| | | | |
|---|-----|-----|-----|
| 290 | 295 | 300 | |
| Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu | | | |
| 305 | 310 | 315 | 320 |
| Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly | | | |
| | 325 | 330 | 335 |
| Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser | | | |
| | 340 | 345 | 350 |
| Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr | | | |
| | 355 | 360 | 365 |
| Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly | | | |
| | 370 | 375 | 380 |
| Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu | | | |
| 385 | 390 | 395 | 400 |
| Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala | | | |
| | 405 | 410 | 415 |
| Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys | | | |
| | 420 | 425 | 430 |
| Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser | | | |
| | 435 | 440 | 445 |
| Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val | | | |
| | 450 | 455 | 460 |
| Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu | | | |
| 465 | 470 | 475 | 480 |
| Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val | | | |
| | 485 | 490 | |

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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 35

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agaatatcac ggc atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc 109

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val

1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157

Leu Phe Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu

15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205

Gly Phe Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe

30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc 253

His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly

45 50 55 60

tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag 301

Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys

65 70 75

gaa aac aag tgt ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc 349

Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile

80 85 90

ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag 397

Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln

95 100 105

aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt 445

Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg

110 115 120

tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca 493

Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser

125 130 135 140

ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc 541

Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly

145 150 155

cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg 589

Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala

160 165 170

aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc 637

Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile
175 180 185

acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg 685
Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu
190 195 200

acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta 730
Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
205 210 215

tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaccatt 790

tatagcatga agccctacat gatcactgca ggatgacct cctcccatcc ttccctttt 850

taggtccctg tcttatacaa ccagagaagt ggggtgttggc caggcacatc ccatctcagg 910

cagcaagaca atctttcact cactgacggc agcagccatg tctctcaaag tggtgaaact 970

aatatctgag catcttttag acaagagagg caaagacaaa ctggatttaa tggcccaaca 1030

tcaaaggggtg aaccaggat atgaatttt gcactttccc attgtcgaat tagtctccag 1090

cctctaaata atgccagtc ttctcccaa agtcaagcaa gagactagt gaagggagtt 1150

ctggggccag gctcactgga ccattgtcac aaccctctgt ttctcttga ctaagtgcc 1210

tggctacagg aattacacag ttctcttct ccaaagggca agatctcatt tcaatttct 1270

tattagaggg ccttattgat gtgttctaag tcttccaga aaaaaactat ccagtgatt 1330

atatcctgat ttcaaccagt cacttagctg ataatcacag taagaagact tctggtatta 1390

tctctctatc agataagatt ttgttaatgt actattttac tcttcaataa ataaaacagt 1450

tt 1452

<210> 36

<211> 219

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15

Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile

| | | |
|---|-----|-----|
| 20 | 25 | 30 |
| Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro | | |
| 35 | 40 | 45 |
| Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met | | |
| 50 | 55 | 60 |
| Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys | | |
| 65 | 70 | 75 |
| Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu | | |
| 85 | 90 | 95 |
| Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu | | |
| 100 | 105 | 110 |
| Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp | | |
| 115 | 120 | 125 |
| Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys | | |
| 130 | 135 | 140 |
| Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser | | |
| 145 | 150 | 155 |
| Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu | | |
| 165 | 170 | 175 |
| Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val | | |
| 180 | 185 | 190 |
| Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys | | |
| 195 | 200 | 205 |
| Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu | | |
| 210 | 215 | |

<210> 37

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

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ctttagagca ca

12